

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/825, 632 A
Source: IFW/6
Date Processed by STIC: 07/06/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/06/2006

PATENT APPLICATION: US/10/825,632A

TIME: 17:26:39

Input Set : A:\FCSB100DIV1SEQ.TXT

Output Set: N:\CRF4\07062006\J825632A.raw

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4 <110> APPLICANT: ABBOTT, Catherine Anne
5      GORRELL, Mark Douglas
7 <120> TITLE OF INVENTION: DIPEPTIDYL PEPTIDASES
10 <130> FILE REFERENCE: FCSB-100-Div. 1
12 <140> CURRENT APPLICATION NUMBER: 10/825,632A
13 <141> CURRENT FILING DATE: 2004-04-15
15 <150> PRIOR APPLICATION NUMBER: US 10/070,464
16 <151> PRIOR FILING DATE: 2002-07-18
18 <150> PRIOR APPLICATION NUMBER: PCT/AU00/01085
19 <151> PRIOR FILING DATE: 2000-09-11
21 <150> PRIOR APPLICATION NUMBER: AU PQ5709
22 <151> PRIOR FILING DATE: 2000-02-18
24 <150> PRIOR APPLICATION NUMBER: AU PQ2762
25 <151> PRIOR FILING DATE: 1999-09-10
27 <160> NUMBER OF SEQ ID NOS: 33
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 882
33 <212> TYPE: PRT
34 <213> ORGANISM: Homo Sapiens
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39 Thr Ala Asp Cys Glu Glu Asn Ile Glu Ser Gln Asp Arg Pro Lys Leu
40          20          25          30
41 Glu Pro Phe Tyr Val Glu Arg Tyr Ser Trp Ser Gln Leu Lys Lys Leu
42          35          40          45
43 Leu Ala Asp Thr Arg Lys Tyr His Gly Tyr Met Met Ala Lys Ala Pro
44          50          55          60
45 His Asp Phe Met Phe Val Lys Arg Asn Asp Pro Asp Gly Pro His Ser
46 65          70          75          80
47 Asp Arg Ile Tyr Tyr Leu Ala Met Ser Gly Glu Asn Arg Glu Asn Thr
48          85          90          95
49 Leu Phe Tyr Ser Glu Ile Pro Lys Thr Ile Asn Arg Ala Ala Val Leu
50          100         105         110
51 Met Leu Ser Trp Lys Pro Leu Leu Asp Leu Phe Gln Ala Thr Leu Asp
52          115         120         125
53 Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg
54          130         135         140
55 Ile Gly Thr Val Gly Ile Ala Ser Tyr Asp Tyr His Gln Gly Ser Gly
56 145         150         155         160
57 Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile Tyr His Val Lys Asp Gly
58          165         170         175

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59 Gly Pro Gln Gly Phe Thr Gln Gln Pro Leu Arg Pro Asn Leu Val Glu
60      180      185      190
61 Thr Ser Cys Pro Asn Ile Arg Met Asp Pro Lys Leu Cys Pro Ala Asp
62      195      200      205
63 Pro Asp Trp Ile Ala Phe Ile His Ser Asn Asp Ile Trp Ile Ser Asn
64      210      215      220
65 Ile Val Thr Arg Glu Glu Arg Arg Leu Thr Tyr Val His Asn Glu Leu
66 225      230      235      240
67 Ala Asn Met Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val
68      245      250      255
69 Leu Gln Glu Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys
70      260      265      270
71 Ala Glu Thr Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu
72      275      280      285
73 Glu Asn Asp Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met
74      290      295      300
75 Leu Glu Thr Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr
76 305      310      315      320
77 Ala Asn Pro Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala
78      325      330      335
79 Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile Gln Pro Phe
80      340      345      350
81 Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr
82      355      360      365
83 Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg Ser Gln Thr
84      370      375      380
85 Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile Pro Val Glu
86 385      390      395      400
87 Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val Pro Asp Ser
88      405      410      415
89 Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile Trp Ile Asn
90      420      425      430
91 Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu Glu Glu Ile
92      435      440      445
93 Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg His Leu Tyr
94      450      455      460
95 Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg Ser Ser Gly
96 465      470      475      480
97 Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys Glu Glu Ile
98      485      490      495
99 Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His Gly Ser Asn
100      500      505      510
101 Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
102      515      520      525
103 Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
104      530      535      540
105 Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
106 545      550      555      560
107 Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys

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108          565          570          575
109 Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
110          580          585          590
111 Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
112          595          600          605
113 Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
114          610          615          620
115 Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
116 625          630          635          640
117 Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
118          645          650          655
119 Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
120          660          665          670
121 Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
122          675          680          685
123 Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
124          690          695          700
125 Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
126 705          710          715          720
127 Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
128          725          730          735
129 Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
130          740          745          750
131 Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
132          755          760          765
133 Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp
134          770          775          780
135 Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu
136 785          790          795          800
137 Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu
138          805          810          815
139 Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu
140          820          825          830
141 Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg
142          835          840          845
143 His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu
144          850          855          860
145 Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys
146 865          870          875          880
147 Val Ile
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152 <211> LENGTH: 3120
153 <212> TYPE: DNA
154 <213> ORGANISM: Homo Sapiens
156 <400> SEQUENCE: 2
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158 cgttcgccgc ctgggttgct accggcgccg ccgccgagga agccactgca accaggaccg 120
159 gagtggaggc ggcgcagcat gaagcggcgc aggcccgctc catagcgcac gtcgggacgg 180
160 tccgggcccgg gcccggggga aggaaaatgc aacatggcag cagcaatgga aacagaacag 240

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161 ctgggtgttg agatatttga aactgcggac tgtgaggaga atattgaatc acaggatcgg 300
162 cctaaattgg agccttttta tgttgagcgg tattcctgga gtcagcttaa aaagctgctt 360
163 gccgatacca gaaaatatca tggctacatg atggctaagg caccacatga tttcatgttt 420
164 gtgaagagga atgatccaga tggacctcat tcagacagaa tctattacct tgccatgtct 480
165 ggtgagaaca gagaaaatac actgttttat tctgaaattc ccaaaactat caatagagca 540
166 gcagtcttaa tgctctcttg gaagcctctt ttggatcttt ttcaggcaac actggactat 600
167 ggaatgtatt ctcgagaaga agaactatta agagaaagaa aacgcattgg aacagtcgga 660
168 attgcttctt acgattatca ccaaggaagt ggaacatttc tgtttcaagc cggtagtgga 720
169 atttatcacg taaaagatgg agggccacaa ggatttacgc aacaaccttt aaggcccaat 780
170 ctagtggaaa ctagttgtcc caacatacgg atggatccaa aattatgccc cgctgatcca 840
171 gactggattg cttttataca tagcaacgat atttggatat ctaacatcgt aaccagagaa 900
172 gaaaggagac tcacttatgt gcacaatgag ctagccaaca tggagaaga tgccagatca 960
173 gctggagtgc ctacctttgt tctccaagaa gaatttgata gatattctgg ctattggtgg 1020
174 tgtccaaaag ctgaaacaac tcccagtggg ggtaaaattc ttagaattct atatgaagaa 1080
175 aatgatgaat ctgaggtgga aattattcat gttacatccc ctatgttgga aacaaggagg 1140
176 gcagattcat tccgttatcc taaaacaggt acagcaaadc ctaaagtcac ttttaagatg 1200
177 tcagaaataa tgattgatgc tgaagggaagg atcatagatg tcatagataa ggaactaatt 1260
178 caaccttttg agattctatt tgaaggagtt gaatatattg ccagagctgg atggactcct 1320
179 gagggaaaat atgcttggtc catcctacta gatcgctccc agactcgctt acagatagtg 1380
180 ttgatctcac ctgaattatt tatcccagta gaagatgatg ttatggaaag gcagagactc 1440
181 attgagtcag tgctgatctc tgtgacgcca ctaattatct atgaagaaac aacagacatc 1500
182 tggataaata tccatgacat ctttcatgtt tttcccaaaa gtcacgaaga ggaaattgag 1560
183 tttatttttg cctctgaatg caaaacaggt ttccgtcatt tatacaaaat tacatctatt 1620
184 ttaaaggaaa gcaaatataa acgatccagt ggtgggctgc ctgctccaag tgatttcaag 1680
185 tgtcctatca aagaggagat agcaattacc agtggatgat ggggaagttct tggccggcat 1740
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188 ctgactgacc gtggctactc acattcttgc tgcacagtc agcactgtga cttctttata 1920
189 agtaagtata gtaaccagaa gaatccacac tgtgtgtccc tttacaagct atcaagtctt 1980
190 gaagatgacc caacttgcaa aacaaaggaa ttttgggcca ccattttgga ttcagcaggt 2040
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195 ggatcctgtc accgagggtt taaatttgaa ggcgccttta aatataaaat ggggtcaaata 2340
196 gaaattgacg atcagggtgga aggactccaa tatctagctt ctcgatatga tttcattgac 2400
197 ttagatcgtg tgggcatcca cggctggtcc tatggaggat acctctccct gatggcatta 2460
198 atgcagaggt cagatatctt cagggttgct attgctgggg cccagtcac tctgtggatc 2520
199 ttctatgata caggatacac ggaacgttat atgggtcacc ctgaccagaa tgaacagggc 2580
200 tattacttag gatctgtggc catgcaagca gaaaagttcc cctctgaacc aaatcgttta 2640
201 ctgctcttac atggtttcct ggatgagaat gtccattttg cacataccag tatattactg 2700
202 agtttttttag tgagggtctg aaagccatat gatttacaga tctatcctca ggagagacac 2760
203 agcataagag ttctgaatc gggagaacat tatgaactgc atcttttgca ctaccttcaa 2820
204 gaaaaccttg gatcacgtat tgctgctcta aaagtgatat aattttgacc tgtgtagaac 2880
205 tctctggtat acactggcta ttttaacaaa tgaggaggtt taatcaacag aaaacacaga 2940
206 attgatcatc acattttgat acctgccatg taacatctac tccgtgaaaat aaatgtggtg 3000
207 ccatgcaggg gtctacgggt tgtggtagta atctaatacc ttaacccac atgctcaaaa 3060
208 tcaaatgata catattctct agagaccag caataccata agaattacta aaaaaaaaaa 3120
211 <210> SEQ ID NO: 3

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212 <211> LENGTH: 310
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo Sapiens
216 <400> SEQUENCE: 3
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219 Ser Tyr Val Asn Pro Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr
220 20 25 30
221 Ser His Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys
222 35 40 45
223 Tyr Ser Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser
224 50 55 60
225 Ser Pro Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr
226 65 70 75 80
227 Ile Leu Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile
228 85 90 95
229 Phe Ser Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr
230 100 105 110
231 Lys Pro His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe
232 115 120 125
233 Ile Tyr Gly Gly Pro Gln Gly Gln Ile Glu Ile Asp Asp Gln Val Glu
234 130 135 140
235 Gly Leu Gln Tyr Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg
236 145 150 155 160
237 Val Gly Ile His Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala
238 165 170 175
239 Leu Met Gln Arg Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro
240 180 185 190
241 Val Thr Leu Trp Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met
242 195 200 205
243 Gly His Pro Asp Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala
244 210 215 220
245 Met Gln Ala Glu Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu
246 225 230 235 240
247 His Gly Phe Leu Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu
248 245 250 255
249 Leu Ser Phe Leu Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr
250 260 265 270
251 Pro Gln Glu Arg His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr
252 275 280 285
253 Glu Leu His Leu Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile
254 290 295 300
255 Ala Ala Leu Lys Val Ile
256 305 310
259 <210> SEQ ID NO: 4
260 <211> LENGTH: 1197
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo Sapiens
264 <400> SEQUENCE: 4

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VERIFICATION SUMMARY

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